

1 AGATGAGTGT GGGGGTGA AGAGTCAAGT TCGGGGCA
 METSerVal GlyArgArg ArgValLysLeu LeuGlyIle
 41 CCGATGATG GCAAAGTCT TCATTATTT GATGIGGAA
 eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu
 81 GTCTCCAAA ACAGTAGCA AGACAAAAT CGAAGGGAG
 ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG
 121 GGTATATAT CCGAAGAG AGGTCTGCA AGCAACCCAG
 lyValIleIle ProLysGlu LysPheTrpLys ProProSe
 161 CAGTCCCGG GGTACTGCA ACAGGGACA GGAAGCTG
 rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu
 201 AACAGTGGT ACAATCCCT CTGACAGG GTGGCAATC
 AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG
 241 AGACAGGGA GGTAGGACA TCTCCAAACA CAGTCACT
 lThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe
 281 GGCATTTGT GAAACAGCT CGAGGTGAT GACAGCTG
 uSerTyrCys GluProAspSer ThrValMET ThrAlaVal
 321 ACAGATTTA ATATCTGCC GACAGATT AAAGACTTC
 ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL
 361 TCTGTATTT GAGTGGCG AATTACTGC TCCTATAGA
 euLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs
 401 TCAACCGAG AAATGTCAA AGAGCCCTT CTACTATTG
 pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu
 441 CGATAAAGT CCGTATTCC ACATTTGCC AGAAGGCAAG
 AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA
 481 CAATCCGGA GTCTGGGGC CGGAAACA ACCTAGGGA
 laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs
 521 CCGACAGTA GTGAGGGCT TCGGTGCG CAGACACC
 nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro
 561 CCGAGGACA ACCACCTCA CTTTGGAC ATGCTAAGT
 ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP
 601 TTGAGGTGA CAGCACCG GACATCTCA TGTGGACTA
 heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTy
 641 TAGAGACACA TCTTCAACC TGACCTGAA GGAAGTCTG
 rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1 (sheet 1 of 2)

641 TTTCCTAGGT GGGTGGGAC TTCTGTCCA GAGCGAGT
 PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP
 721 TTGTCTTCAA GGGCATGAT GAGGTTTTC TGAACACCA
 heValPheLys GlyAspAsp AspValPheVal AsnThrHi
 761 TCACATCCTT AATTACTTCA ATAGCTTATC CAAGAGCAAA
 sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys
 801 GCGAAGACT TGTTCATAGG TGGGTGATC CACAATGCTG
 AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG
 841 GGGCTCAGG GGTATAGAAA CTCAGTACT ACATCCGAGA
 LyProHisArg AspLysLys LeuLysTyrTyr IleProGl
 881 AGTCTCTTAC ACCGGGCTT ACCACGCTA TCGGGGGCT
 uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly
 921 GGTGGTTCC TGTACTCCG GGGCTTCC TTGAGGCTT
 GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT
 961 ACAGTCCGAC TGGGGGGTCT CTCCTCTCC CTATTGATCA
 yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs
 1001 TGTCTATAG GGTATGTGCTT TTGAGAACT GGGCTTGT
 pValTyrThr GlyMetCysLeu GlnLysLeu GlyLeuVal
 1041 CCGAGGAGC ACAAGGCTT CAGGACATT GATATTGAG
 ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG
 1081 AGAAAAATAA GAAAAATATT TGTCTCTATA TAGACTAAT
 LuLysAsnLys LysAsnIle CysSerTyrIle AspLeuME
 1121 GTTAGTACAT AGCAGAAAC CTCAGAGAT GATTGATATC
 TLeuValHis SerArgLysPro GlnGluMET IleAspIle
 1161 TGTCTCTAGT TCGAAGTCC TAATTAAAA TGTCTA
 TrpSerGlnLeu GlnSerPro AsnLeuLys Cys

FIG. 1 (sheet 2 of 2)

```

MAX--PQKV-----LRL-LL--V
      10              20              30
MSVGP-RLV-----K-L
MA--S-SC-----Y-
MAP-----AVLTALPNRMSLPS-KWSL
MQSKHRL-----LFCIL--V
MLQWPRRHCCFAKMTWNAKRSIFPTHITIGV

LSLVKLLXXXFXFLKH--W-----
      40              50              60
LGILMMANV-IV-IVEVSKNSSQDKNGKGG
LSVVC-----ASA-----
L-----LSSLSSLV-----
LPLILLVVGYCGLITHLH-----
LSIVFIFAMELEFN-HD-LPGRAGFKENPV

--F--F--D-----TWY
      70              80              90
VIIPKEKFWK-PSTPRAYWNREQEKLNRWY
-----LWY
ELNFERHSHY-----
TYTERG-FRSTKSETNHSSLR-----NIXK

LSIP--LRPQTGSXSXSXXLSHL-Y-----N
      100             110             120
NPILNRVANGT-ELATSPNTSHLSMCEPDS
LSIT--P-TS-YTG-KPFSHI-----
LSLPHY-----
-----ENDDTGGGA-SGLDKFAV-----
ETVPOQLPPOTATNENNTDLSPOQGVGTLES

TVXRYNXXFXNNXXTP-----PINSXXFEF
      130             140             150
TVMTAVTDFFNNLPDFFKDFLLYLRCRNYSL
TVARKNFTFGNIRP-----PHSPHF
VIEPVMWMYF-YEYE-----LYRQDFRF
-----LRVPEFTAHV
TLSANGSIY-EKGIG-----HPNHYH-KY

LIDEPYKCKKK-PFLVLLIKSXPGXFXARQ
      160             170             180
LIPQFKKCAK-PFEL-AIP-LIPHARRC
LINEFNCEFNIPFLI-I-STTHKE-DARC
TLRFHNSHQNFIIVT-RHSDVKARC
PVGQEAR-----TMEI-AVGNRRPE
LINEFEKQEQE-SPP-I-IAAEEQIEER

AIRETWGXEXNFXGIXVXRVELLGKXA-EX
      190             200             210
AIRESWGRETNVGNOTVVEVFLLGFTTPFD
AIRETWGDFNNHKGK-KIATLFLLGNNR--
AIPVTWGEKKSWWGYEMLTFELGQQA-FR
AIFRTWGYEGRESDVHLRVELLGTAEDESE
SIFQTWGNFSLAPG-QIT-IFELLSI--K

XDPXLXXMVEXESRXHGDIIQQDFLDITYFN
      220             230             240
NHEDLSDMLKFEEDKQDILMWNRYR-FFR
-LFVLNQMVQESQIFHDIIVEDFISYHN
E-KTIALSLFDEHVLVJDI-RDDFISTYNN
KQ-----AWESH-EHCDILCADSTCAYEN
LNGYIQRAILEESRQYHDTIOGEYIDTYVY

LTLKTLMGMRWVATFCPXA EYVMKTDSDVF
      250             260             270
SLKEVLFLLRWVSISSCHDAFVFFGLDDCVF
LTKTTEGMRWVATFCISKAKYVWVAVD-SIF
LTKTIFAERWVMEFCNAKVIMKTTTDOV
NTLKTMLGHPWASEQFNRSFYLFLVLD EYY
LTKTLMGMNWVATYCHHIPVWVWVDSFME

VNTXNLLNKLKPSLSHRXXLFTGY-VIXG
      280             290             300
VNTHHIINHYLNSLCKKAKKDFIG-DVIHN
VNMONLIYHLL-ESTKPRRYFTGN-VIN
IN-GNIVKYL--N-NHSEKFFFTVPLTDN
VSAKNVIFKFLGRGROFQOPELFAGHAFQT
VNT EYHINERID-PP-HNY-ETN-LMR

```

FIG. 2 (sheet 1 of 2)

YGPYRDKFSKWTXKDLYPFVYPPYCSGG
 310 320 330
 AGFHRDDEKLRYYTTEVFT-GYPPYAGG
 -GFIIRIVRSKMYMERIY:DSNYPF
 S-YPGFHHKNNHISYQEVPIKWFPPY
 -SILPHKFSKWTVSLEEYPFDRWPPVTA
 VAFNENFDSKWTMIFPLYESERVEVF
 GYIFSGDLAERLYKASLHVRLHLEDVYVG
 340 350 360
 FLYC-PIALHISSTSRHLYPID
 VHSADVALLIY-TT
 HCGDVPVYEMMSKPIKF
 AFGLSOKALROAVLPPFRFD
 VGHNDIAKIFVGI
 ICLXKLGIDPXXPXG--FNHW-KXXKSXC
 370 380 390
 MCLQKLGGLVSEKHKCFRTSDISEKKNKNI
 LCLRLGLHGFQNSQ--FNHW-FMAYLC
 -YNLHKVTHICEDTNLFFLY-RIHLDV
 VALHAGISLOHCDD--RFHRPAYGPD
 IANIRTDVPPNEFV--RVSY
 SYSRVIAV4OF-SPEEMIRIWNXL--KNL
 400 410 420
 YIDLMLVSR-KQEMDINSOI-SP
 RYRRVITVHAI-UPHEHIDMSKHI
 QLRPVIAHGF-SKEITTFQVML--RT
 YSSVITASHFGDPEETVWE--
 KYCHLITSHGF-QISELTKYHMHQNH
 XC-----Y-----
 430
 KCC
 RCT
 TCC-----H
 -CC-----RSANY-----A
 ACANAAKEXAGRVRHRKLH

FIG. 2 (sheet 2 of 2)

FIG. 3

ATGATTTCGC CTCAGCCTTT ACTGGTATT TTAGAAATT
 METIleOysPro SerAlaLeu LeuValIle LeuArgAsnL
 41 TATACGGGA AGAAAAATC ATTTCACAG AGATCCTCA
 eIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs
 81 TTGATTGAA TTAGGATGA AAAAGGGAA TATTCAGTTC
 nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu
 121 ACAACTCTG CAATCAGTGA TGCATTAAA GAAATCGATA
 ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS
 161 GTAGTGTGCT CAATGTGCT GTACCGGGG AGACGGGATC
 erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe
 201 AGGGAGTCC AGCTTCATCA ATACCTGAG AGGCATTGGG
 rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly
 241 AATGAGAAG AGGTGCTCC TAAACTGGG GTGGTGGAGG
 AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV
 281 TACCATCGA AGACATCCA TACAACACC CCAATATACC
 alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr
 321 CAATGGGTT TTTCGGGAC TGGCTGGAT TGGAGGACA
 cAsnValVal PheTyrAspLeu ProGlyIle GlySerThr
 361 AATTTCGAC CAAACACTA CCGGAGAAA ATGAAGTCT
 AsnPheProPro AsnThrTyr LeuGluLys METLysPheT
 401 ATGAGTAGA TTCTTCATT ATTATTTCG CCACAGGCT
 yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh
 441 CAGAAAAAT GATATAGCA TTGCCAAGC AATCAGCATG
 eLysLysAsn AspIleAspIle AlaLysAla IleSerMET
 481 ATGAGAAGG AATCTACTT CCGCAGAAC AGGTGGACT
 METLysLysGlu PheTyrPhe ValArgThr LysValAspS
 521 CTGACATAAC AAATGAGCA GATGGCAAC CTCAAACCTT
 erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh
 561 TGCACAAGAA AAGGTCTCC AGGACATCC CCTTAAGTCT
 eAspLysGlu LysValLeuGln AspIleArg LeuAsnOys
 601 CTGACACCTT TTAGGGGAA TGGCATTGCT GAGCCACAA
 ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI
 641 TCTTCTGCT CTCTACAAA AATGTTTGT ACTATGACTT
 lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4 (sheet 1 of 2)

581 CCCCCCTCCG ATGGACAAGC TCATAAGTGA CCCCCCTATC
 eProValLeu METAspLysLeu IleSerAsp LeuProIle
 721 TCCAGGAGAC ACAATTTTAT GCCTCCCTTA CCCAATATCA
 TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT
 761 CAGATTCAGT CATGAAAAG AAGGCGCAAT TTCGCAAGCA
 hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGI
 801 RAGGATTTCG CTGGAAGGAT TTCCTGCTCA CCTAGTGAAT
 nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn
 841 ATCATCCCTT CTCGCGCTT TCCCTGGAC AGTGATTTCG
 IleIleProSer LeuIhrPhe LeuLeuAsp SerAspLeuG
 881 AGCTCTCTCA GAAAGCATG AAATCTCTCC GCATGTGTT
 LuIhrLeuLys LysSerMET LysPheTyrArg ThrValPh
 921 TCGAGTCCAT CAAACTCTT TCGGAGATT AGCTAGGAC
 eGlyValAsp GluIhrSerLeu GlnArgLeu AlaArgAsp
 961 TCGGAATAG AGGTGGTCA CGTGGAGCC ATGATAAAAT
 TrpGluIleGlu ValAspGln ValGluAla METIleLysS
 1001 CTCCTCCCTT GTTCAAACT ACAGATGAG AAACAATACA
 erProAlaVal PheLysPro ThrAspGluGlu ThrIleGI
 1041 AGAAGGCTT TCAAGATATA TTCAGGATT CTGTTCGCT
 nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla
 1081 AATGGTACT TACTTCTTA AAATAGTTT CTAAAGAAA
 AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI
 1121 TATTTTACT GAAATATAT TTCCTGACA TGGTGACTCA
 lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGI
 1161 CGATGCTAAA ACTCTCTTA AAGAGATAG TTAAAGAAC
 uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn
 1201 PG

FIG. 4 (sheet 2 of 2)

[illegible]

FIG. 5

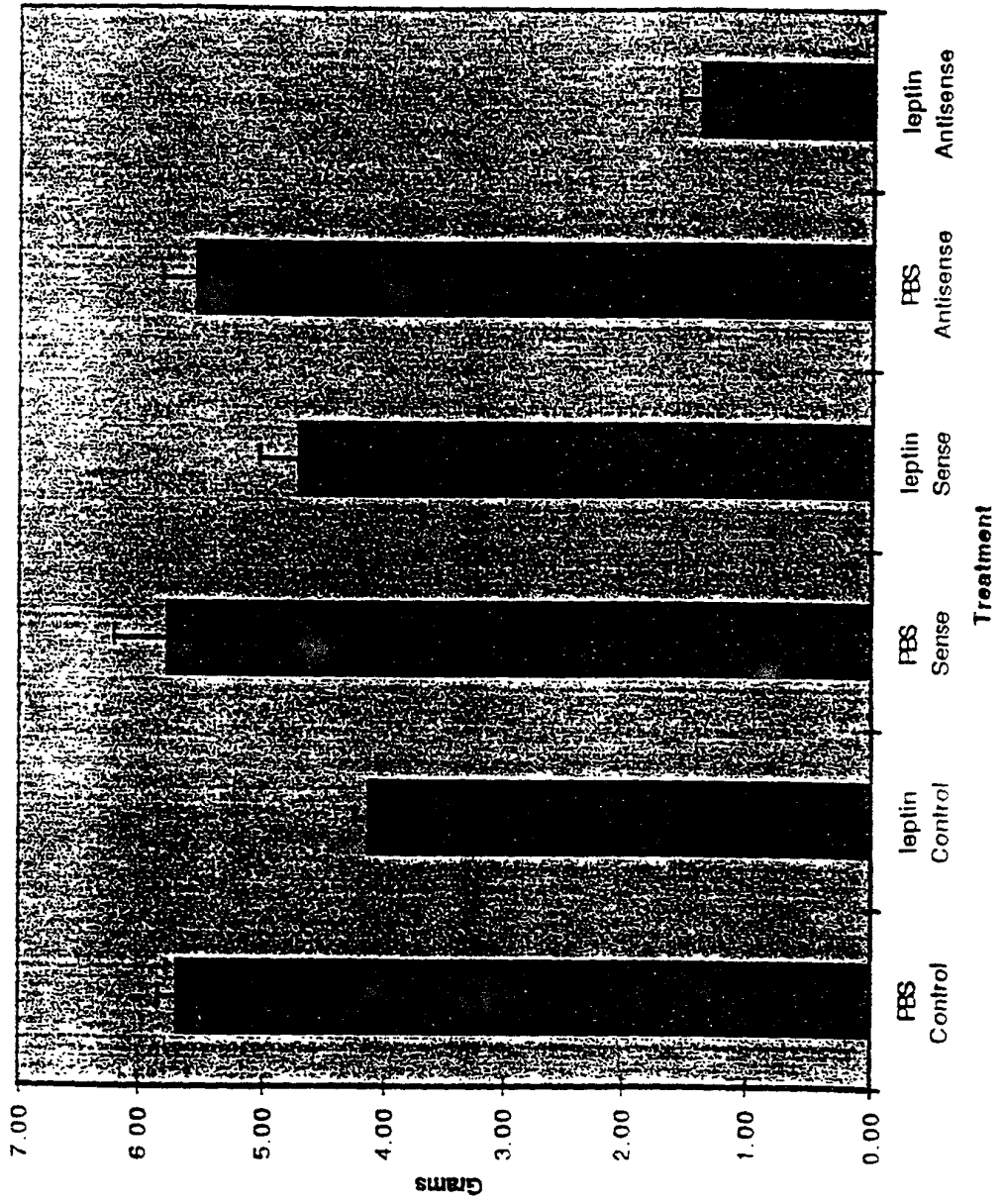


FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGGCCCGCCGTC
CGGGGCGCCGCGCATGGAGCGTGAGCTGCCGCCGGTCGCCGGGCTGAGCCGC
GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAAT**T**GAGTGTTGGA
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCGGTGGTTACGGGT
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG
CAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT
TGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGA
GTCTTCCTGCTGGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG
TAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGATGACGATGTT
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC
ACCCTATGCAGGGGGAGGGGGGTTTCTCTACTCCGGCCACCTGGCCCTGAGG
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATTTGATGACGTTTATAC
TGGAATGTGCCTTCAGAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT
CAGTTGCAGAGTGCTCATTTAAAATGCT**T**AAAATAGATACAAACTCAATTTKG
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATAACCCATTTANGGCC
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN
NLPDRFKDFLLYLRCRNYSLIDQPDKCAKKPFLLAIAKSLTPHFARRQAIRESWG
QESNAGNQTVVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNRYRDTFFNL
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV
IHNAGPHRDKKLKYYIPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY
PIDDVYTGMCLOKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM
IDIWSQLQSAHLKC

Sequence

START

201 CCCCCCCCCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTGAGACGT 260
 5 CCCCCCCCCCGAGCTGGAGGTGTCCCTAGACAAGGTATGAGAGATGAGTGTGGGGCGT 64

251 CGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTATTTTATTATG 320
 65 CGAAGAGTCAAGTTGCTGGGCATCCTGATGATGGCAAATGTCTTCATTTATTTGATTGTG 124

321 GAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAATACCCAAA 380
 125 GAAGTCTCCAAAACAGTAGCCAAGACAAAAATGGAAAAGGGAGGAGTAATAATCCCGAAA 184

381 GAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCGAGAGCAAGAGAAG 440
 185 GAGAAGTTCTGGAAGCCACCCAGCACTCCCGGGCATACTGGAACAGGGAACAGGAGAAG 244

441 CTGAACCGGGCAGTACAACCCCATCCTGAGCATGCTGACCAACCAGACGGGGGAGGGGGC 500
 245 CTGAACAGGTGGTACAATCCCATCTTGAACAGGGTGGCCAATCAGACAGGGGAGCTAGCC 304

501 AGGCTCTCCAATATAAGCCATCTGAACACTGCGAACCTGACCTGAGGGTCACGTGGGTG 560
 305 ACATCTCCAAACACAAGTCACCTGAGCTATTGTGAACAGACTCGACGGTCATGACAGCT 364

561 GTTACGGGTTTTTAACAACCTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 620
 365 GTGACAGATTTTAATAATCTGCCGGACAGATTTAAAGACTTTCTCTGTATTTGAGATGC 424

621 CGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCTTGTG 680
 425 CGGAATTACTCGCTGCTTATAGATCAACCGAAGAAATGTGCAAAGAAGCCCTTCTTACTA 484

681 CTGGCGATTAAAGTCCCTCACTCCACATTTTCCAGAAGGCAAGCAATCCGGGAATCCTGG 740
 485 TTGGCGATAAAGTCCCTCATTCACATTTTCCAGAAGGCAAGCAATCCGGGAGTCTTGG 544

741 GGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTCTTCCTGCTGGGCCAGACA 800
 545 GGCCGAGAAACCAACGTAGGGAACCAGACAGTAGTGAGGGTCTTCCTGTTGGGCAAGACA 604

801 CCCCCAGAGGACAACCACCCGACCTTTTCCAGATATGCTGAAATTTGAGAGTGAGAAGCAC 860
 605 CCCCCAGAGGACAACCACCCGACCTTTTCCGACATGCTTAAGTTTGAGAGTGACAAGCAC 664

861 CAAGACATTCTTATGTGGAACCTACAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTG 920
 665 CAGGACATCCTCATGTGGAACCTATAGAGACACATTCTTCAACCTGTCCCTGAAGGAAGTG 724

921 CTGTTTCTCAGGTGGGTAAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGAT 980
 725 CTGTTTCTTAGGTGGGTGAGCACTTCCTGTCCAGACGAGAGTTTGTCTTCAAGGGCGAT 784

981 GACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACC 1040
 785 GATGACGTGTTTGTGAACACCCATCACATCCTTAATTACTTGAATAGCTTATCCAAGAGC 844

1041 AAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGGGATAAG 1100
 845 AAAGCCAAAGACTTGTTCATAGGTGACGTGATCCACAATGCTGGGCCTCACCGGGATAAG 904

FIG. 9 (10F2)

[illegible]

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLIDQPKKCAKKPFLLLAIKSLIPHFARRQAIRESWGRETNVGNQTVVRVF
***** :*.* *****

VFKGDDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYSGLY
VFKGDDDDVFVNTHHILNYLNSLSKSKAKDLFIGDVIHNAGPHRDKKLKYYIPEVFYTG
***** : : :

```
PPYAGGGGFLYSGHLALRLYHITDOVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGPLALRLYSATSRVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE
***** ~*****
```

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKKNICSYIDLMLVHSRKPQEMIDIWSQLQSPNLKC
*****.*****.***** *****.***

FIG 10

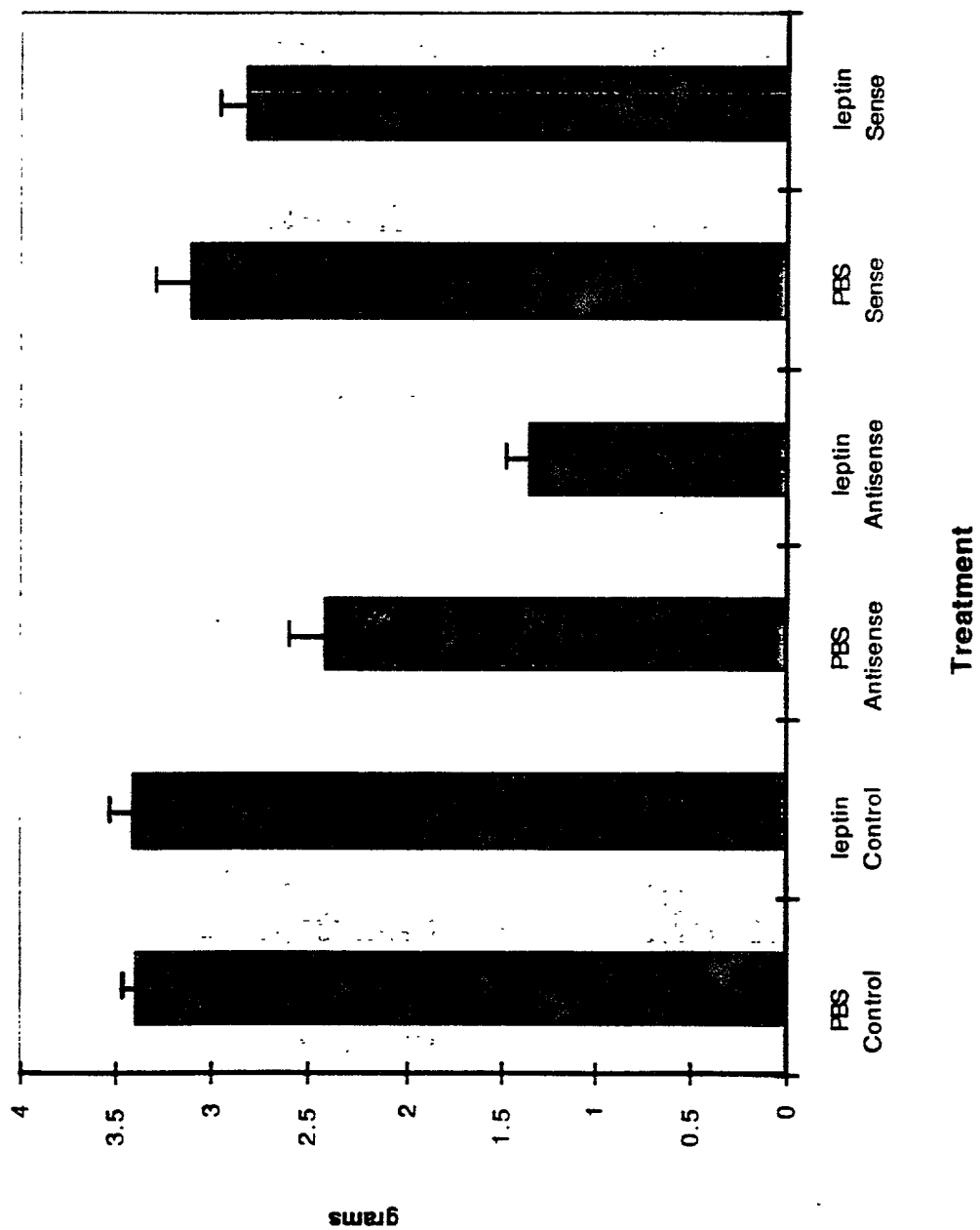


Fig. 11